

Amendments to the Specification

Please make the following amendments to the application prior to examination and consideration.

Replace the paragraph beginning at page 5, line 26 with the following.

Figure 3 is a Pfam analysis of the polypeptide (SEQ ID NO:38) encoded by human EST AA315020 (SEQ ID NO:4).

Replace the paragraph beginning at page 6, line 1 with the following.

Figure 4B shows an alignment of amino acids 28-131 28-128 of SEQ ID NO:3 with amino acids 1-101 of Acc. No. AY 007220, an S-100 type binding protein, and consensus sequence (SEQ ID NO:40).

Replace the paragraph beginning at page 6, line 4 with the following.

Figure 4C shows an alignment of amino acids 28-131 15-118 of SEQ ID NO:6 with amino acids 1-101 1-104 of Acc. No. AY007220, and consensus sequence (SEQ ID NO:49).

Replace the paragraph beginning at page 6, line 19 with the following.

Figure 7 is a CAP alignment and consensus of human assembly 6567721-3-frag (SEQ ID NO:5) compared to human EST AA315020 (SEQ ID NO:48; the complementary strand sequence of SEQ ID NO:4), and CuraGen assembly 65677221 (SEQ ID NO:37).

Replace the paragraph beginning at page 10, line 1, with the following.

Figs. 4B-4E show comparisons of portions of the amino acid sequences shown in Table 3 (SEQ ID NO:3) and Table 6 (SEQ ID NO:6) to S-100-type calcium binding proteins. Fig 4B shows an alignment of amino acids 28-131 28 - 128 of SEQ ID NO:3 with amino acids 1-101 of Acc. No. AY007220 (SEQ ID NO:39) [[a]] an S-100 type calcium binding protein. Identical or conserved amino acid residues are indicated in black shading. These residues may be required to preserve structural or functional properties of the protein. Amino acids shaded in gray can be mutated to a residue with comparable steric and/or chemical properties without altering protein

structure or function, e.g., L to V, I or M. Non-highlighted amino acid can potentially be mutated to a much broader extent without altering structure or function.

Replace the paragraph beginning at page 10, line 10, with the following.

Fig. 4C shows an alignment of amino acids ~~28-131~~ 15-118 of SEQ ID NO:6 with amino acids ~~1-104~~ 1-104 of Acc. No. AY007220. Shading is as explained for FIG. 4B.